

SEQUENCE LISTING



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Kobayashi, Tohru
Koyama, Shingo
Sato, Tsuyoshi

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<170> PatentIn version 3.2

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Ala Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
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			180					185					190			
ggt	tcc	tat	gca	gat	aat	att	aac	cac	gtt	gca	cag	ttc	tct	tcc	cgt	624
Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg	
		195					200					205				
ggc	ccg	aca	aaa	gat	ggg	cga	atc	aag	cct	gat	gtc	atg	gcg	cca	ggg	672
Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly	
	210					215					220					
aca	tac	att	tta	tca	gca	aga	tct	tct	ctt	gca	ccc	gat	tcc	tcc	ttc	720
Thr	Tyr	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	
225					230					235					240	
tgg	gcg	aat	cat	gac	agc	aaa	tat	gcc	tat	atg	ggt	gga	acg	tcc	atg	768
Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	
				245					250					255		
gca	aca	ccg	att	gtt	gcg	ggg	aat	gtt	gca	cag	ctc	cgt	gag	cat	ttt	816
Ala	Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	
			260					265					270			
gtg	aaa	aat	aga	gga	atc	act	cct	aag	cct	tcc	cta	ttg	aaa	gca	gct	864
Val	Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala	
		275					280					285				
ttg	att	gca	ggt	gct	gct	gat	gtt	gga	ttg	ggt	tat	ccg	aac	gga	aac	912
Leu	Ile	Ala	Gly	Ala	Ala	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Asn	Gly	Asn	
		290				295					300					
caa	gga	tgg	ggc	cga	gtg	acc	ctg	gat	aaa	tcg	ttg	aac	gtt	gcc	tat	960
Gln	Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	
305					310					315					320	
gtg	aac	gaa	tcc	agt	gcc	cta	tca	act	agc	caa	aaa	gcg	aca	tat	acc	1008
Val	Asn	Glu	Ser	Ser	Ala	Leu	Ser	Thr	Ser	Gln	Lys	Ala	Thr	Tyr	Thr	
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ttt	act	gca	acg	gcg	ggc	aag	cca	ttg	aaa	atc	tcc	ctg	gta	tgg	tcg	1056

Phe	Thr	Ala	Thr	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Ser		
			340					345					350				
gat	gcc	cct	gca	agc	act	act	gct	tct	gta	acc	ctg	gtc	aat	gat	ttg		1104
Asp	Ala	Pro	Ala	Ser	Thr	Thr	Ala	Ser	Val	Thr	Leu	Val	Asn	Asp	Leu		
		355					360					365					
gat	ttg	gtc	att	aca	gca	cca	aac	gga	aca	aga	tat	gtc	ggg	aat	gac		1152
Asp	Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Thr	Arg	Tyr	Val	Gly	Asn	Asp		
	370						375				380						
ttc	tca	gca	cca	ttt	gac	aat	aac	tgg	gat	ggc	cgc	aat	aac	gta	gaa		1200
Phe	Ser	Ala	Pro	Phe	Asp	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu		
385					390					395					400		
aat	gta	ttt	att	aat	tcg	ccc	caa	agt	gga	aca	tat	acc	att	gag	gtg		1248
Asn	Val	Phe	Ile	Asn	Ser	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Ile	Glu	Val		
				405					410					415			
caa	gca	tat	aat	gtg	ccg	gtt	gga	cca	caa	aac	ttc	tcg	ttg	gca	att		1296
Gln	Ala	Tyr	Asn	Val	Pro	Val	Gly	Pro	Gln	Asn	Phe	Ser	Leu	Ala	Ile		
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gtg	aac																1302
Val	Asn																

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 <212> PRT
 <213> Bacillus sp. KSM-kp9860

<400> 12

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Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Ile	Val	Ala	Val	Ala	Asp	Thr	Gly		
			20					25					30				
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly		
		35					40					45					
Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp		
	50					55					60						
Thr	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Gly		

65					70					75				80	
Ala	Thr	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser
				85					90					95	
Ile	Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Gln
			100					105					110		
Thr	Leu	Phe	Ser	Gln	Ala	Phe	Ser	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn
		115					120					125			
Ser	Trp	Gly	Ala	Ala	Val	Asn	Gly	Ala	Tyr	Thr	Thr	Asp	Ser	Arg	Asn
	130					135						140			
Val	Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Thr	Ile	Leu	Phe	Ala	Ala
145					150					155					160
Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala
				165					170					175	
Lys	Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Leu	Arg	Pro	Ser	Phe
			180					185					190		
Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg
		195					200					205			
Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly
	210					215					220				
Thr	Tyr	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe
225					230					235					240
Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met
				245					250					255	
Ala	Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe
			260					265					270		
Val	Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala

275

280

285

Leu Ile Ala Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn
 290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr
 305 310 315 320

Val Asn Glu Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr
 325 330 335

Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
 340 345 350

Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
 355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp
 370 375 380

Phe Ser Ala Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu
 385 390 395 400

Asn Val Phe Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val
 405 410 415

Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile
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Val Asn

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 <221> CDS
 <222> (1) .. (1302)

<223> Protease 9865

<400> 13

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tac ggg ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg	96
Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly	
20 25 30	
ctt gat aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgg ggg	144
Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly	
35 40 45	
aaa att act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat	192
Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp	
50 55 60	
acg aat ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc	240
Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly	
65 70 75 80	
tcc act aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct	288
Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser	
85 90 95	
atc atg gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa	336
Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln	
100 105 110	
acc tta ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac	384
Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn	
115 120 125	
tcc tgg gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat	432
Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn	
130 135 140	
gtg gat gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc	480
Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala	
145 150 155 160	
ggg aat gaa gga ccg aac ggc gga acc atc agt gca cca ggc aca gct	528
Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala	
165 170 175	
aaa aat gca ata aca gtc gga gct acg gaa aac ctc cgc cca agc ttc	576
Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe	
180 185 190	
ggg tct tat gcg gac aat atc aac cat gtg gca cag ttc tct tca cgt	624

Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg	
		195					200					205				
gga	ccg	aca	aag	gat	gga	cgg	atc	aaa	ccg	gat	gtc	atg	gca	ccg	gga	672
Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly	
	210					215					220					
acg	ttc	ata	cta	tca	gca	aga	tct	tct	ctt	gca	ccg	gat	tcc	tcc	ttc	720
Thr	Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	
	225				230					235					240	
tgg	gcg	aac	cat	gac	agt	aaa	tat	gca	tac	atg	ggc	gga	acg	tcc	atg	768
Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	
				245					250					255		
gct	aca	ccg	atc	gtt	gct	gga	aac	gtg	gca	cag	ctt	cgt	gag	cat	ttt	816
Ala	Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	
			260					265					270			
gtg	aaa	aac	aga	ggc	atc	aca	cca	aag	cct	tct	cta	tta	aaa	gcg	gca	864
Val	Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala	
		275					280					285				
ctg	att	gcc	ggc	gca	gca	gac	atc	ggc	ctt	ggc	tac	ccg	aac	ggc	aac	912
Leu	Ile	Ala	Gly	Ala	Ala	Asp	Ile	Gly	Leu	Gly	Tyr	Pro	Asn	Gly	Asn	
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caa	gga	tgg	gga	cga	gtg	aca	ttg	gat	aaa	tcc	cta	aac	gtt	gcc	tat	960
Gln	Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	
	305				310					315					320	
gtg	aac	gag	tcc	agt	tct	cta	tcc	acc	agc	caa	aaa	gcg	acg	tac	tcg	1008
Val	Asn	Glu	Ser	Ser	Ser	Leu	Ser	Thr	Ser	Gln	Lys	Ala	Thr	Tyr	Ser	
				325					330					335		
ttt	act	gct	act	gcc	ggc	aag	cct	ttg	aag	atc	tcc	ctg	gta	tgg	tct	1056
Phe	Thr	Ala	Thr	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Ser	
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gat	gcc	cct	gcg	agc	aca	act	gct	tcc	gta	acg	ctt	gtc	aat	gac	ctg	1104
Asp	Ala	Pro	Ala	Ser	Thr	Thr	Ala	Ser	Val	Thr	Leu	Val	Asn	Asp	Leu	
		355					360					365				
gac	ctt	gtc	att	acc	gct	cca	aat	ggc	aca	caa	tat	gtt	gga	aat	gac	1152
Asp	Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Thr	Gln	Tyr	Val	Gly	Asn	Asp	
	370					375					380					
ttt	act	tcg	cca	tac	aat	aat	aac	tgg	gat	ggc	cgc	aat	aac	gta	gaa	1200
Phe	Thr	Ser	Pro	Tyr	Asn	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu	
	385				390					395					400	
aat	gta	ttt	att	aat	gcg	cca	caa	agc	ggg	acg	tat	aca	att	gag	gta	1248

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val
 405 410 415

cag gct tat aac gta ccg gtt gga cca cag acc ttc tcg ttg gca att 1296
 Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile
 420 425 430

gtg aac 1302
 Val Asn

<210> 14
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 <212> PRT
 <213> Bacillus sp. KSM-9865
 <400> 14

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser
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Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
 20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
 35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
 50 55 60

Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
 65 70 75 80

Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
 85 90 95

Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln
 100 105 110

Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn
 115 120 125

Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn

130					135					140						
Val	Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Thr	Ile	Leu	Phe	Ala	Ala	
145					150					155					160	
Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	
				165					170					175		
Lys	Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Leu	Arg	Pro	Ser	Phe	
			180					185					190			
Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg	
		195					200					205				
Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly	
	210					215					220					
Thr	Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	
225					230					235					240	
Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	
				245					250					255		
Ala	Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	
			260					265					270			
Val	Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala	
		275					280					285				
Leu	Ile	Ala	Gly	Ala	Ala	Asp	Ile	Gly	Leu	Gly	Tyr	Pro	Asn	Gly	Asn	
	290					295					300					
Gln	Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	
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Val	Asn	Glu	Ser	Ser	Ser	Leu	Ser	Thr	Ser	Gln	Lys	Ala	Thr	Tyr	Ser	
				325					330					335		
Phe	Thr	Ala	Thr	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Ser	

340

345

350

Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
 355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp
 370 375 380

Phe Thr Ser Pro Tyr Asn Asn Asn Trp Asp Gly Arg Asn Asn Val Glu
 385 390 395 400

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val
 405 410 415

Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile
 420 425 430

Val Asn

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 <212> DNA
 <213> Bacillus sp. D-6

<220>
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 <222> (1)..(1299)
 <223> Protease E-1

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 tac gga cta tat gga caa ggt caa gta gtt gca gta gcg gat acg ggt 96
 Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly
 20 25 30
 tta gat aca ggt cgt aac gat agt tct atg cat gaa gca ttc cgt ggg 144
 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
 35 40 45
 aaa att aca gct ctt tac gcg tta gga aga act aac aat gca aat gat 192

Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp	
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Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Ala	
65					70					75					80	
tta	aat	aaa	gga	atg	gct	ccg	caa	gct	aac	tta	gtc	ttc	caa	tct	att	288
Leu	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	Ile	
				85					90					95		
atg	gat	agc	agc	gga	gga	tta	gga	gga	tta	cca	tcg	aat	tta	aat	acg	336
Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Asn	Thr	
			100					105					110			
tta	ttt	agt	caa	gct	tgg	aat	gct	ggc	gct	aga	att	cat	act	aac	tct	384
Leu	Phe	Ser	Gln	Ala	Trp	Asn	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn	Ser	
		115					120					125				
tgg	ggg	gcc	cca	gta	aat	gga	gcg	tac	act	gct	aac	tcg	aga	caa	gtg	432
Trp	Gly	Ala	Pro	Val	Asn	Gly	Ala	Tyr	Thr	Ala	Asn	Ser	Arg	Gln	Val	
	130					135					140					
gat	gag	tat	gtt	cga	aac	aat	gat	atg	acg	gta	ctt	ttt	gca	gct	gga	480
Asp	Glu	Tyr	Val	Arg	Asn	Asn	Asp	Met	Thr	Val	Leu	Phe	Ala	Ala	Gly	
145					150					155					160	
aat	gaa	gga	cct	aac	tct	gga	aca	att	agc	gct	cca	ggg	aca	gcg	aaa	528
Asn	Glu	Gly	Pro	Asn	Ser	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	Lys	
				165					170					175		
aat	gcc	att	acg	gtc	ggc	gca	acg	gaa	aac	tac	cga	cca	agt	ttt	ggg	576
Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Tyr	Arg	Pro	Ser	Phe	Gly	
			180					185					190			
tca	att	gca	gat	aac	cct	aat	cat	atc	gca	caa	ttt	tca	tcg	aga	gga	624
Ser	Ile	Ala	Asp	Asn	Pro	Asn	His	Ile	Ala	Gln	Phe	Ser	Ser	Arg	Gly	
		195					200					205				
gct	acg	aga	gat	gga	cga	att	aaa	cca	gac	gta	aca	gct	cct	gga	aca	672
Ala	Thr	Arg	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Thr	Ala	Pro	Gly	Thr	
	210					215					220					
ttt	ata	tta	tca	gca	cgc	tct	tct	tta	gca	cca	gac	tct	tcg	ttt	tgg	720
Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp	
225					230					235					240	
gcg	aat	tat	aac	agt	aag	tat	gcg	tat	atg	ggc	ggg	acc	tct	atg	gcg	768
Ala	Asn	Tyr	Asn	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala	
				245					250					255		
aca	cct	ata	gtt	gcg	ggg	aat	gtc	gcg	caa	tta	cgc	gag	cat	ttt	ata	816

Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Ile	
			260					265					270			
aaa	aat	aga	gga	att	aca	cct	aaa	cct	tcc	tta	ata	aaa	gct	gca	ctt	864
Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Ile	Lys	Ala	Ala	Leu	
		275					280					285				
atc	gct	ggg	gct	act	gat	gtt	ggg	tta	gga	tat	cca	agt	ggg	gac	caa	912
Ile	Ala	Gly	Ala	Thr	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Ser	Gly	Asp	Gln	
	290					295					300					
ggc	tgg	ggg	cgt	gtt	act	tta	gat	aaa	tcg	tta	aat	gta	gcg	tat	gtc	960
Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val	
305					310					315					320	
aat	gaa	gca	act	gca	tta	aca	aca	gga	caa	aaa	gca	acg	tat	tcg	ttc	1008
Asn	Glu	Ala	Thr	Ala	Leu	Thr	Thr	Gly	Gln	Lys	Ala	Thr	Tyr	Ser	Phe	
				325					330					335		
caa	acg	caa	gcg	ggg	aaa	cca	tta	aaa	atc	tcg	tta	gta	tgg	aca	gat	1056
Gln	Thr	Gln	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Thr	Asp	
			340					345					350			
gca	cct	gga	agt	aca	aca	gca	tct	tat	aca	cta	gtt	aat	gat	tta	gat	1104
Ala	Pro	Gly	Ser	Thr	Thr	Ala	Ser	Tyr	Thr	Leu	Val	Asn	Asp	Leu	Asp	
		355					360					365				
cta	gtt	att	act	gct	ccg	aat	gga	caa	aaa	tat	gta	ggg	aat	gat	ttt	1152
Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Gln	Lys	Tyr	Val	Gly	Asn	Asp	Phe	
	370					375					380					
agt	tat	cct	tat	gat	aat	aat	tgg	gat	ggg	cgc	aac	aat	gtt	gag	aac	1200
Ser	Tyr	Pro	Tyr	Asp	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu	Asn	
385					390					395					400	
gta	ttt	ata	aac	gct	ccg	caa	tct	gga	acg	tat	aca	att	gag	gtt	caa	1248
Val	Phe	Ile	Asn	Ala	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Ile	Glu	Val	Gln	
				405					410					415		
gcg	tat	aac	gtt	cca	tct	gga	cca	cag	cgt	ttc	tca	cta	gct	atc	gta	1296
Ala	Tyr	Asn	Val	Pro	Ser	Gly	Pro	Gln	Arg	Phe	Ser	Leu	Ala	Ile	Val	
			420					425					430			
cat																1299
His																

<210> 16
 <211> 433
 <212> PRT
 <213> Bacillus sp. D-6

<400> 16

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn
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Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly
20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala
65 70 75 80

Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile
85 90 95

Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr
100 105 110

Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser
115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val
130 135 140

Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly
145 150 155 160

Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys
165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly
180 185 190

Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly
195 200 205

Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr
210 215 220

Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp
225 230 235 240

Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala
245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile
260 265 270

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu
275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Ser Gly Asp Gln
290 295 300

Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val
305 310 315 320

Asn Glu Ala Thr Ala Leu Thr Thr Gly Gln Lys Ala Thr Tyr Ser Phe
325 330 335

Gln Thr Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp
340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp
355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe
370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln
405 410 415

Ala	Tyr	Asn	Val	Pro	Ser	Gly	Pro	Gln	Arg	Phe	Ser	Leu	Ala	Ile	Val
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His

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<220>
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 <222> (1)..(1299)
 <223> Gene name Ya,

Protease Ya

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1				5					10					15		
tac	gga	tta	tat	gga	caa	ggg	caa	gta	gtt	gca	gta	gcg	gac	aca	ggc	96
Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Val	Val	Ala	Val	Ala	Asp	Thr	Gly	
			20					25					30			
tta	gat	aca	ggg	cgt	aac	gat	agt	tct	atg	cat	gaa	gca	ttc	cgc	ggg	144
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly	
		35					40					45				
aaa	atc	aca	gct	ctt	tac	gcg	tta	gga	aga	act	aat	aat	gcg	agt	gat	192
Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Ser	Asp	
	50					55					60					
ccg	aat	ggg	cat	ggc	aca	cat	gta	gca	ggg	tct	gta	ctt	ggg	aat	gct	240
Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Ala	
65					70					75					80	
tta	aat	aaa	gga	atg	gct	ccg	caa	gct	aac	tta	gtc	ttc	caa	tct	att	288
Leu	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	Ile	
				85					90					95		
atg	gat	agc	agc	gga	gga	tta	ggg	ggc	tta	cca	tcg	aac	tta	aat	acg	336
Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Asn	Thr	
			100					105					110			
tta	ttt	agt	caa	gct	tgg	aat	gct	gga	gca	aga	att	cat	act	aac	tct	384
Leu	Phe	Ser	Gln	Ala	Trp	Asn	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn	Ser	

115						120						125							
tgg	gga	gcc	cca	gta	aat	gga	gcg	tac	act	gct	aac	tcg	aga	caa	gtg	432			
Trp	Gly	Ala	Pro	Val	Asn	Gly	Ala	Tyr	Thr	Ala	Asn	Ser	Arg	Gln	Val				
130						135						140							
gat	gaa	tat	gtt	cga	aat	aat	gat	atg	acg	gta	ctt	ttt	gca	gct	ggt	480			
Asp	Glu	Tyr	Val	Arg	Asn	Asn	Asp	Met	Thr	Val	Leu	Phe	Ala	Ala	Gly				
145						150						155						160	
aat	gaa	ggt	cct	aat	tca	gga	aca	att	agt	gct	cca	ggt	aca	gcg	aaa	528			
Asn	Glu	Gly	Pro	Asn	Ser	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	Lys				
165						170						175							
aat	gct	att	acg	gtc	ggc	gca	acg	gaa	aac	tat	cgc	cca	agc	ttc	ggt	576			
Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Tyr	Arg	Pro	Ser	Phe	Gly				
180						185						190							
tcg	ata	gca	gat	aac	cca	aat	cat	att	gca	caa	ttt	tca	tcg	aga	gga	624			
Ser	Ile	Ala	Asp	Asn	Pro	Asn	His	Ile	Ala	Gln	Phe	Ser	Ser	Arg	Gly				
195						200						205							
gct	acg	agg	gat	gga	cga	att	aag	cct	gac	gta	aca	gct	cct	gga	aca	672			
Ala	Thr	Arg	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Thr	Ala	Pro	Gly	Thr				
210						215						220							
ttt	att	tta	tca	gca	cgt	tct	tcc	tta	gct	cca	gac	tct	tcg	ttt	tgg	720			
Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp				
225						230						235						240	
gcg	aat	tat	aac	agt	aaa	tac	gcg	tat	atg	ggc	ggt	acc	tcc	atg	gcg	768			
Ala	Asn	Tyr	Asn	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala				
245						250						255							
aca	cct	att	gtt	gca	ggg	aat	gtc	gcg	caa	tta	cgt	gag	cat	ttt	ata	816			
Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Ile				
260						265						270							
aaa	aat	aga	ggt	att	act	cct	aag	cct	tct	tta	ata	aaa	gct	gca	ctt	864			
Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Ile	Lys	Ala	Ala	Leu				
275						280						285							
atc	gct	ggt	gct	act	gat	gtt	ggt	tta	gga	tat	cct	aat	ggt	gac	caa	912			
Ile	Ala	Gly	Ala	Thr	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Asn	Gly	Asp	Gln				
290						295						300							
ggc	tgg	ggg	cgt	gtt	act	cta	aat	aaa	tcg	tta	aat	gta	gcg	tat	gtc	960			
Gly	Trp	Gly	Arg	Val	Thr	Leu	Asn	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val				
305						310						315						320	
aat	gaa	gca	act	gca	tta	gcc	aca	gga	caa	aaa	gca	acg	tat	tcg	ttc	1008			
Asn	Glu	Ala	Thr	Ala	Leu	Ala	Thr	Gly	Gln	Lys	Ala	Thr	Tyr	Ser	Phe				

325

330

335

caa gca caa gcg ggt aaa cct tta aaa atc tcg tta gta tgg aca gat 1056
 Gln Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp
 340 345 350

gct cct gga agt aca act gca tct tat aca cta gtt aat gat tta gat 1104
 Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp
 355 360 365

cta gtt att act gct ccg aat gga caa aaa tat gta gga aat gat ttt 1152
 Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe
 370 375 380

agt tat cct tat gat aat aac tgg gat ggt cgc aac aat gtt gag aac 1200
 Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
 385 390 395 400

gta ttt ata aac gct ccg caa tct gga acg tat ata att gag gtt caa 1248
 Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Ile Ile Glu Val Gln
 405 410 415

gcg tat aat gta cca tct ggc cca cag cgt ttc tca cta gct atc gta 1296
 Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val
 420 425 430

cat 1299
 His

<210> 18
 <211> 433
 <212> PRT
 <213> Bacillus sp. Y

<400> 18

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn
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Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly
 20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
 35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Ser Asp
 50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala
65 70 75 80

Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile
85 90 95

Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr
100 105 110

Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser
115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val
130 135 140

Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly
145 150 155 160

Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys
165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly
180 185 190

Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly
195 200 205

Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr
210 215 220

Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp
225 230 235 240

Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala
245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile
260 265 270

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu
 275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Asn Gly Asp Gln
 290 295 300

Gly Trp Gly Arg Val Thr Leu Asn Lys Ser Leu Asn Val Ala Tyr Val
 305 310 315 320

Asn Glu Ala Thr Ala Leu Ala Thr Gly Gln Lys Ala Thr Tyr Ser Phe
 325 330 335

Gln Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp
 340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp
 355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Ile Ile Glu Val Gln
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val
 420 425 430

His

<210> 19
 <211> 1299
 <212> DNA
 <213> Bacillus SD521

<220>
 <221> CDS

<222> (1) .. (1299)

<223> Gene name SD-521, protease SD521

<400> 19

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Asn	Asp	Val	Ala	Arg	Gly	Ile	Val	Lys	Ala	Asp	Val	Ala	Gln	Asn	Asn	
1				5					10					15		

tac	gga	cta	tat	gga	caa	ggg	caa	gta	gtt	gca	gta	gcg	gat	acg	ggg	96
Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Val	Val	Ala	Val	Ala	Asp	Thr	Gly	
			20					25					30			

tta	gat	aca	ggg	cgt	aac	gat	agt	tct	atg	cat	gaa	gca	ttc	cgt	ggg	144
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly	
		35					40					45				

aaa	att	aca	gct	ctt	tac	gcg	tta	gga	aga	act	aac	aat	gca	aat	gat	192
Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp	
	50					55					60					

ccg	aat	ggg	cat	ggg	acg	cat	gta	gca	ggg	tct	gta	ctt	ggg	aat	gct	240
Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Ala	
65					70					75					80	

tta	aat	aaa	gga	atg	gct	ccg	caa	gct	aac	tta	gtc	ttc	caa	tct	att	288
Leu	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	Ile	
				85					90					95		

atg	gat	agc	agc	gga	gga	tta	ggg	gga	tta	cca	tcg	aat	ttg	aat	acg	336
Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Asn	Thr	
			100					105					110			

tta	ttt	agt	caa	gct	tgg	aat	gct	ggg	gct	aga	att	cat	act	aac	tct	384
Leu	Phe	Ser	Gln	Ala	Trp	Asn	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn	Ser	
		115					120					125				

tgg	ggg	gct	cca	gta	aat	gga	gcg	tac	act	gct	aac	tcg	aga	caa	gtg	432
Trp	Gly	Ala	Pro	Val	Asn	Gly	Ala	Tyr	Thr	Ala	Asn	Ser	Arg	Gln	Val	
	130					135					140					

gat	gag	tat	gtt	cga	aat	aat	gat	atg	acg	gta	ctt	ttt	gca	gca	ggg	480
Asp	Glu	Tyr	Val	Arg	Asn	Asn	Asp	Met	Thr	Val	Leu	Phe	Ala	Ala	Gly	
145					150					155					160	

aat	gaa	ggg	cct	aat	tca	gga	aca	att	agt	gct	cca	ggc	aca	gcg	aaa	528
Asn	Glu	Gly	Pro	Asn	Ser	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	Lys	
				165					170					175		

aat	gcc	att	acg	gtc	ggc	gca	acg	gaa	aac	tat	cgc	ccg	agc	ttc	ggg	576
Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Tyr	Arg	Pro	Ser	Phe	Gly	
			180					185					190			

tca	tta	gca	gat	aac	cca	aat	cat	atc	gca	caa	ttt	tca	tca	aga	gga	624
Ser	Leu	Ala	Asp	Asn	Pro	Asn	His	Ile	Ala	Gln	Phe	Ser	Ser	Arg	Gly	
		195					200					205				
gct	acg	aga	gat	gga	cga	att	aaa	cca	gac	gta	aca	gct	cct	gga	aca	672
Ala	Thr	Arg	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Thr	Ala	Pro	Gly	Thr	
	210					215					220					
ttt	att	tta	tca	gca	cgt	tct	tcc	tta	gcc	cca	gac	tct	tcg	ttt	tgg	720
Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp	
225					230					235					240	
gcg	aat	tat	aac	agt	aag	tat	gcg	tac	atg	ggc	ggg	acc	tct	atg	gcg	768
Ala	Asn	Tyr	Asn	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala	
				245					250					255		
aca	cct	ata	gtt	gcg	ggg	aat	gtc	gcg	caa	tta	cgc	gag	cat	ttt	ata	816
Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Ile	
			260					265					270			
aaa	aat	aga	gga	att	aca	cct	aaa	cct	tcc	tta	ata	aaa	gct	gca	ctt	864
Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Ile	Lys	Ala	Ala	Leu	
		275					280					285				
atc	gct	ggg	gct	act	gat	gtt	ggg	tta	gga	tat	cca	agt	ggg	gac	caa	912
Ile	Ala	Gly	Ala	Thr	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Ser	Gly	Asp	Gln	
	290					295					300					
ggc	tgg	ggg	cgt	gtt	act	cta	gat	aaa	tcg	tta	aat	gta	gcg	tat	gtc	960
Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val	
305					310					315					320	
aat	gaa	gca	act	gca	tta	gca	aca	gga	caa	aaa	gca	acg	tat	tcg	ttc	1008
Asn	Glu	Ala	Thr	Ala	Leu	Ala	Thr	Gly	Gln	Lys	Ala	Thr	Tyr	Ser	Phe	
				325					330					335		
caa	gca	caa	gcg	ggg	aaa	cct	tta	aaa	atc	tcg	tta	gta	tgg	aca	gat	1056
Gln	Ala	Gln	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Thr	Asp	
			340					345					350			
gca	cct	gga	agt	aca	act	gca	tct	tat	aca	cta	gtt	aat	gat	tta	gat	1104
Ala	Pro	Gly	Ser	Thr	Thr	Ala	Ser	Tyr	Thr	Leu	Val	Asn	Asp	Leu	Asp	
		355					360					365				
cta	gtt	att	act	gct	ccg	aat	gga	caa	aaa	tat	gta	gga	aat	gat	ttt	1152
Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Gln	Lys	Tyr	Val	Gly	Asn	Asp	Phe	
	370					375					380					
agt	tat	cct	tat	gat	aat	aac	tgg	gat	ggg	cgc	aac	aat	gtt	gag	aac	1200
Ser	Tyr	Pro	Tyr	Asp	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu	Asn	
385					390					395					400	

gta	ttt	ata	aac	gct	ccg	caa	tct	gga	acg	tat	aca	att	gag	gtt	caa	1248
Val	Phe	Ile	Asn	Ala	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Ile	Glu	Val	Gln	
				405					410					415		

gcg	tat	aat	gta	cca	tct	ggc	cca	cag	cgt	ttc	tca	cta	gct	atc	gta	1296
Ala	Tyr	Asn	Val	Pro	Ser	Gly	Pro	Gln	Arg	Phe	Ser	Leu	Ala	Ile	Val	
			420					425					430			

cat																1299
His																

<210> 20
 <211> 433
 <212> PRT
 <213> Bacillus SD521

<400> 20

Asn	Asp	Val	Ala	Arg	Gly	Ile	Val	Lys	Ala	Asp	Val	Ala	Gln	Asn	Asn
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Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Val	Val	Ala	Val	Ala	Asp	Thr	Gly
			20					25					30		

Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly
		35					40					45			

Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp
	50					55					60				

Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Ala
65					70					75					80

Leu	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	Ile
				85					90					95	

Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Asn	Thr
			100					105					110		

Leu	Phe	Ser	Gln	Ala	Trp	Asn	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn	Ser
		115					120					125			

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val
 130 135 140

Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly
 145 150 155 160

Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys
 165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly
 180 185 190

Ser Leu Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly
 195 200 205

Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr
 210 215 220

Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp
 225 230 235 240

Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala
 245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile
 260 265 270

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu
 275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Ser Gly Asp Gln
 290 295 300

Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val
 305 310 315 320

Asn Glu Ala Thr Ala Leu Ala Thr Gly Gln Lys Ala Thr Tyr Ser Phe
 325 330 335

Gln Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp
 340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp
 355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val
 420 425 430

His

<210> 21
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Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser	
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tat ggt tta tat ggg caa ggg caa gtg gtt gca gta gcg gat acc gga	96
Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly	
20 25 30	
ctg gat aca ggg cgt aat gac agc tcg atg cat gaa gcg ttc cga gga	144
Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly	
35 40 45	

aag Lys 50	att Ile	acc Thr	gcg Ala	ata Ile	tat Tyr	gcc Ala 55	ctt Leu	gga Gly	aga Arg	aca Thr	aac Asn 60	aac Asn	gcc Ala	aat Asn	gat Asp	192
cca Pro 65	aac Asn	gga Gly	cac His	ggg Gly	acg Thr 70	cat His	gtt Val	gcc Ala	gga Gly	tct Ser 75	gtt Val	tta Leu	gga Gly	aac Asn	ggg Gly 80	240
act Thr	tcg Ser	aat Asn	aaa Lys	ggg Gly 85	atg Met	gct Ala	cca Pro	caa Gln	gct Ala 90	aac Asn	tta Leu	gtt Val	ttc Phe	caa Gln 95	tct Ser	288
gtt Val	atg Met	gac Asp	agc Ser 100	aat Asn	ggc Gly	gga Gly	ctt Leu	ggc Gly 105	gga Gly	ctg Leu	cct Pro	tcc Ser	aat Asn 110	gta Val	agt Ser	336
aca Thr	tta Leu 115	ttc Phe	agc Ser	cag Gln	gca Ala	tat Tyr	agt Ser 120	gcc Ala	ggg Gly	gcc Ala	aga Arg	atc Ile 125	cat His	acg Thr	aac Asn	384
tca Ser 130	tgg Trp	gga Gly	gcg Ala	cct Pro	gta Val	aac Asn 135	gga Gly	gcg Ala	tac Tyr	act Thr	act Thr 140	gat Asp	tcc Ser	aga Arg	aac Asn	432
gta Val 145	gac Asp	gat Asp	tat Tyr	gtt Val	cgt Arg 150	aaa Lys	aat Asn	gat Asp	atg Met	gcg Ala 155	gtt Val	ctt Leu	ttt Phe	gca Ala 160	gcg Ala	480
ggg Gly	aac Asn	gaa Glu	ggg Gly 165	ccg Pro	aat Asn	ggc Gly	ggc Gly	aca Thr	atc Ile 170	agt Ser	gct Ala	cct Pro	ggg Gly 175	acc Thr	gcg Ala	528
aag Lys	aat Asn	gct Ala	atc Ile 180	aca Thr	gta Val	ggg Gly	gca Ala	aca Thr 185	gaa Glu	aac Asn	ctg Leu	cgc Arg	cca Pro 190	agc Ser	ttt Phe	576
gga Gly	tct Ser	tat Tyr 195	gct Ala	gac Asp	aac Asn	atc Ile	aat Asn 200	cat His	gta Val	gca Ala	cag Gln	ttt Phe 205	tcc Ser	tcc Ser	cgc Arg	624
gga Gly 210	cct Pro	aca Thr	aag Lys	gat Asp	gga Gly	cgt Arg 215	atc Ile	aaa Lys	ccg Pro	gac Asp	gta Val 220	atg Met	gca Ala	cca Pro	gga Gly	672
aca Thr 225	ttt Phe	att Ile	tta Leu	tcg Ser	gca Ala 230	aga Arg	tct Ser	tct Ser	ttg Leu 235	gct Ala	ccg Pro	gac Asp	tcc Ser	tca Ser	ttc Phe 240	720
tgg Trp	gca Ala	aac Asn	cat His	gac Asp 245	agc Ser	aaa Lys	tat Tyr	gct Ala	tat Tyr 250	atg Met	ggg Gly	gga Gly	aca Thr	tcc Ser 255	atg Met	768

gcg aca ccg att gta gct ggt aac gtt gca cag tta cgt gaa cat ttc	816
Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe	
260 265 270	
atc aaa aac aga gga atc act cct aaa cca tcc ttg ctg aaa gca gct	864
Ile Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala	
275 280 285	
ctt att gcc gga gca act gat atc ggt ctt ggc tat ccg agt gga aac	912
Leu Ile Ala Gly Ala Thr Asp Ile Gly Leu Gly Tyr Pro Ser Gly Asn	
290 295 300	
caa gga tgg gga aga gta aca ttg gac aag tca ctt aat gta gct ttc	960
Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Phe	
305 310 315 320	
gta aat gaa aca agc tct tta tct act aac caa aag gct acg tat tca	1008
Val Asn Glu Thr Ser Ser Leu Ser Thr Asn Gln Lys Ala Thr Tyr Ser	
325 330 335	
ttt act gca caa tca ggc aaa cct ttg aag att tca ttg gtt tgg tct	1056
Phe Thr Ala Gln Ser Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser	
340 345 350	
gat gca ccg gca agt act tcc gca tcg gtt aca ttg gtg aat gat ctg	1104
Asp Ala Pro Ala Ser Thr Ser Ala Ser Val Thr Leu Val Asn Asp Leu	
355 360 365	
gat ctg gtg att aca gct cca aat gga aca aag tat gtt gga aac gac	1152
Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Lys Tyr Val Gly Asn Asp	
370 375 380	
ttt act gct ccc tat gat aat aac tgg gat gga cgt aac aat gta gag	1200
Phe Thr Ala Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu	
385 390 395 400	
aac gtg ttt atc aat gct ccg caa agc gga acg tat aca gtt gag gta	1248
Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Val Glu Val	
405 410 415	
cag gct tac aat gtt cca caa ggg ccg cag gcg ttt tct ttg gct att	1296
Gln Ala Tyr Asn Val Pro Gln Gly Pro Gln Ala Phe Ser Leu Ala Ile	
420 425 430	
gtg aac	1302
Val Asn	

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 <211> 434
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<213> NCIB12289

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Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser
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Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly
20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Ile Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
65 70 75 80

Thr Ser Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
85 90 95

Val Met Asp Ser Asn Gly Gly Leu Gly Gly Leu Pro Ser Asn Val Ser
100 105 110

Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn
115 120 125

Ser Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
130 135 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Ala Val Leu Phe Ala Ala
145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala
165 170 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe
180 185 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg
195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
210 215 220

Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe
225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
260 265 270

Ile Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala
275 280 285

Leu Ile Ala Gly Ala Thr Asp Ile Gly Leu Gly Tyr Pro Ser Gly Asn
290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Phe
305 310 315 320

Val Asn Glu Thr Ser Ser Leu Ser Thr Asn Gln Lys Ala Thr Tyr Ser
325 330 335

Phe Thr Ala Gln Ser Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
340 345 350

Asp Ala Pro Ala Ser Thr Ser Ala Ser Val Thr Leu Val Asn Asp Leu
355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Lys Tyr Val Gly Asn Asp
370 375 380

Phe Thr Ala Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu
385 390 395 400

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Val Glu Val
 405 410 415

Gln Ala Tyr Asn Val Pro Gln Gly Pro Gln Ala Phe Ser Leu Ala Ile
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Val Asn

<210> 23
 <211> 433
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Phe Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
 20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
 35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
 50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala
 65 70 75 80

Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile
 85 90 95

Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ala Asn Leu Gln Thr
 100 105 110

Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser
 115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val

130						135										140
Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Thr	Ile	Leu	Phe	Ala	Ala	Gly	
145					150					155					160	
Asn	Glu	Gly	Pro	Gly	Ser	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	Lys	
				165					170					175		
Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Leu	Arg	Pro	Ser	Phe	Gly	
			180					185					190			
Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg	Gly	
		195					200					205				
Pro	Thr	Arg	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly	Thr	
	210					215					220					
Tyr	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp	
225					230					235					240	
Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala	
				245					250					255		
Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Val	
			260					265					270			
Lys	Asn	Arg	Gly	Val	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala	Leu	
		275					280					285				
Ile	Ala	Gly	Ala	Ala	Asp	Val	Gly	Leu	Gly	Phe	Pro	Asn	Gly	Asn	Gln	
	290					295					300					
Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Phe	Val	
305					310					315					320	
Asn	Glu	Thr	Ser	Pro	Leu	Ser	Thr	Ser	Gln	Lys	Ala	Thr	Tyr	Ser	Phe	
				325					330					335		
Thr	Ala	Gln	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Ser	Asp	

340

345

350

Ala Pro Gly Ser Thr Thr Ala Ser Leu Thr Leu Val Asn Asp Leu Asp
355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Thr Lys Tyr Val Gly Asn Asp Phe
370 375 380

Thr Ala Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Val Glu Val Gln
405 410 415

Ala Tyr Asn Val Pro Val Ser Pro Gln Thr Phe Ser Leu Ala Ile Val
420 425 430

His